In the Specification:

Please replace the paragraph beginning at page 5, line 17 of the specification with the following rewritten paragraph:

--Figures 1A-1D show construction and expression of mutant Vpr molecules. Figure 1A shows an amino acid sequence comparison of Vpr of HIV-1 (SEQ ID NO: 1) and 2/SIV (SEQ ID NO:2) and Vpx of HIV-2/SIV (SEQ ID NO:3). Numbers denote positions of amino acid residues for each protein sequence provided. Figure 1B shows expression plasmids for the synthesis of mutant Vpr molecules were generated by overlap Polymerase Chain Reaction (PCR) at the indicated codons. PCR-amplified mutant vpr gene fragments were digested with *HindIII and XhoI* and ligated to pCDNA3 vector to produce Vpr mutant expression plasmids. VPR wt is SEQ ID NO:4; E21,24P is SEQ ID NO:5; αL-A is SEQ ID NO:6; A30S is SEQ ID NO:7; A30L is SEQ ID NO:8; A59P is SEQ ID NO:9; L64S is SEQ ID NO:10; L67S is SEQ ID NO:11; L68S is SEQ ID NO:12; H71C is SEQ ID NO:13; H71Y is SEQ ID NO:14; G75A is SEQ ID NO:15; C76S is SEQ ID NO:16; and HXB2 is SEQ ID NO:17. Figure 1C shows recombinant vaccinia virus (vTF7-3) infected HeLa cells were transfected with wild type and mutant vpr expression plasmids. Transfected cells were labeled with S^{35} protein labeling mix for 2 hours and the cell-associated Vpr proteins were immunoprecipitated with anti-Vpr antiserum as described in Materials and Methods. Immunoprecipitates were analyzed by SDS-12% PAGE. The designation of the Vpr plasmids is indicated at the top. Figure 1D shows the secondary structure of Vpr (SEQ ID NO:18) was calculated using the program *nnpredict* (Kneller, D.G. et al., *J. Mol. Biol.*, **1990**, *214:* 171-182.). *nnpredict* is a program that predicts the secondary structure type for each residue in an amino acid sequence based on the prediction of a two-layer, feed-forward neural network. H is helical, E is extended and dash (-) is undefined. αL-A, L64S, and H71C display the same secondary profile as the Vpr wild-type, suggesting the importance of the Leu residues on the hydrophobic face and His in the C-terminus. Introduction of proline-residue in E21, E24 and A59 disrupt the respective helical domains.--